GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:44:36 ; Search time 146 Seconds
(without alignments)
413.953 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguuauuacagagucuguauagcuguacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	34	3	US-09-363-939A-93	Sequence 93, Appl
2	34	100.0	34	3	US-09-363-939A-115	Sequence 115, App
3	34	100.0	34	3	US-09-363-939A-121	Sequence 121, App
4	34	100.0	34	3	US-09-363-939A-171	Sequence 171, App
5	34	100.0	34	3	US-09-363-939A-172	Sequence 172, App
6	34	100.0	34	3	US-09-363-939A-173	Sequence 173, App
7	34	100.0	34	3	US-09-363-939A-174	Sequence 174, App
8	34	100.0	34	3	US-09-363-939A-175	Sequence 175, App
9	34	100.0	34	3	US-09-363-939A-176	Sequence 176, App
10	34	100.0	34	3	US-09-363-939A-177	Sequence 177, App
11	34	100.0	34	3	US-09-363-939A-178	Sequence 178, App
12	34	100.0	34	3	US-09-363-939A-179	Sequence 179, App
13	34	100.0	34	3	US-09-363-939A-180	Sequence 180, App
14	34	100.0	34	3	US-09-363-939A-181	Sequence 181, App
15	34	100.0	34	3	US-09-363-939A-182	Sequence 182, App
16	34	100.0	34	3	US-09-363-939A-183	Sequence 183, App
17	34	100.0	34	3	US-09-363-939A-184	Sequence 184, App
18	34	100.0	34	3	US-09-363-939A-185	Sequence 185, App
19	34	100.0	34	3	US-09-363-939A-186	Sequence 186, App
20	34	100.0	34	3	US-09-791-301-93	Sequence 93, Appl
21	34	100.0	34	3	US-09-791-301-115	Sequence 115, App
22	34	100.0	34	3	US-09-791-301-121	Sequence 121, App
23	34	100.0	34	3	US-09-791-301-171	Sequence 171, App
24	34	100.0	34	3	US-09-791-301-172	Sequence 172, App
25	34	100.0	34	3	US-09-791-301-173	Sequence 173, App
26	34	100.0	34	3	US-09-791-301-174	Sequence 174, App
27	34	100.0	34	3	US-09-791-301-175	Sequence 175, App
28	34	100.0	34	3	US-09-791-301-176	Sequence 176, App
29	34	100.0	34	3	US-09-791-301-177	Sequence 177, App
30	34	100.0	34	3	US-09-791-301-178	Sequence 178, App
31	34	100.0	34	3	US-09-791-301-179	Sequence 179, App
32	34	100.0	34	3	US-09-791-301-180	Sequence 180, App
33	34	100.0	34	3	US-09-791-301-181	Sequence 181, App
34	34	100.0	34	3	US-09-791-301-182	Sequence 182, App
35	34	100.0	34	3	US-09-791-301-183	Sequence 183, App
36	34	100.0	34	3	US-09-791-301-184	Sequence 184, App
37	34	100.0	34	3	US-09-791-301-185	Sequence 185, App
38	34	100.0	34	3	US-09-791-301-186	Sequence 186, App
39	34	100.0	36	3	US-09-363-939A-92	Sequence 92, Appl
40	34	100.0	36	3	US-09-363-939A-114	Sequence 114, App
41	34	100.0	36	3	US-09-791-301-92	Sequence 92, Appl
42	34	100.0	36	3	US-09-791-301-114	Sequence 114, App
43	34	100.0	37	3	US-09-363-939A-116	Sequence 116, App
44	34	100.0	37	3	US-09-791-301-116	Sequence 116, App
45	34	100.0	43	3	US-09-363-939A-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-363-939A-93
; Sequence 93, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F.
US-09-363-939A-93

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||

```
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 2
US-09-363-939A-115
; Sequence 115, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 115
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F.
US-09-363-939A-115

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 3
US-09-363-939A-121
; Sequence 121, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 121
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F.
US-09-363-939A-121

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 4
US-09-363-939A-171
; Sequence 171, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-171
```

```
  Query Match           100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 5
US-09-363-939A-172
; Sequence 172, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 172
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'OCH3;
;   OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-172

  Query Match           100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 6
US-09-363-939A-173
; Sequence 173, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 173
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-4 are 2'OCH3; linkage at positions 34 and 35 is
;   OTHER INFORMATION: 3'-3'.
US-09-363-939A-173

  Query Match           100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 7
US-09-363-939A-174
; Sequence 174, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 174
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 5, 8, and 11 are 2'OCH3; linkage at positions 34
;   OTHER INFORMATION: and 35 is 3'-3'.
US-09-363-939A-174

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 8
US-09-363-939A-175
; Sequence 175, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 175
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a' and g's at positions
;   OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
;   OTHER INFORMATION: is 3'-3'.
US-09-363-939A-175

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 9
US-09-363-939A-176
; Sequence 176, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 176
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 20, 22 and 24 are 2'-OCH3; linkage at positions 34
;   OTHER INFORMATION: and 35 is 3'-3'.
US-09-363-939A-176

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 10
US-09-363-939A-177
; Sequence 177, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
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; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
; OTHER INFORMATION: 25, 28 and 30 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
US-09-363-939A-177

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||
Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 11
US-09-363-939A-178
; Sequence 178, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; g at position 20 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-178

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||
Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 12
US-09-363-939A-179
; Sequence 179, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a at position 22 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-179

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||
Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 13
US-09-363-939A-180
; Sequence 180, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23

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;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 180
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a at position 24 is
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-180

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 14
US-09-363-939A-181
; Sequence 181, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 181
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-5, 8, 11, 25 and 30 are 2'-OCH3; linkage at
;   OTHER INFORMATION: positions 34 and 35 is 3'-3'.
US-09-363-939A-181

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 15
US-09-363-939A-182
; Sequence 182, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
;  APPLICANT:  Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION:  High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE:  NEX87
;  CURRENT APPLICATION NUMBER: US/09/363,939A
;  CURRENT FILING DATE:  1999-07-29
;  PRIOR APPLICATION NUMBER:  09/046,247
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  08/458,424
;  PRIOR FILING DATE:  1995-06-02
;  PRIOR APPLICATION NUMBER:  07/714,131
;  PRIOR FILING DATE:  1991-06-10
;  PRIOR APPLICATION NUMBER:  07/931,473
;  PRIOR FILING DATE:  1992-08-17
;  PRIOR APPLICATION NUMBER:  07/964,624
;  PRIOR FILING DATE:  1992-10-21
;  PRIOR APPLICATION NUMBER:  08/117,991
;  PRIOR FILING DATE:  1993-09-08
;  PRIOR APPLICATION NUMBER:  07/536,428
;  PRIOR FILING DATE:  1990-06-11
;  NUMBER OF SEQ ID NOS:  216
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 182
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
;   OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-182

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


Search completed: December 27, 2005, 16:45:24
Job time : 146 secs
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:58:35 ; Search time 815 Seconds
(without alignments)
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Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguuauuacagagucuguauagcuguacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	34	3	US-09-791-301-93	Sequence 93, Appl
2	34	100.0	34	3	US-09-791-301-115	Sequence 115, App
3	34	100.0	34	3	US-09-791-301-121	Sequence 121, App
4	34	100.0	34	3	US-09-791-301-171	Sequence 171, App
5	34	100.0	34	3	US-09-791-301-172	Sequence 172, App
6	34	100.0	34	3	US-09-791-301-173	Sequence 173, App
7	34	100.0	34	3	US-09-791-301-174	Sequence 174, App
8	34	100.0	34	3	US-09-791-301-175	Sequence 175, App
9	34	100.0	34	3	US-09-791-301-176	Sequence 176, App
10	34	100.0	34	3	US-09-791-301-177	Sequence 177, App
11	34	100.0	34	3	US-09-791-301-178	Sequence 178, App
12	34	100.0	34	3	US-09-791-301-179	Sequence 179, App
13	34	100.0	34	3	US-09-791-301-180	Sequence 180, App
14	34	100.0	34	3	US-09-791-301-181	Sequence 181, App
15	34	100.0	34	3	US-09-791-301-182	Sequence 182, App
16	34	100.0	34	3	US-09-791-301-183	Sequence 183, App
17	34	100.0	34	3	US-09-791-301-184	Sequence 184, App
18	34	100.0	34	3	US-09-791-301-185	Sequence 185, App
19	34	100.0	34	3	US-09-791-301-186	Sequence 186, App
20	34	100.0	34	8	US-10-718-833-12	Sequence 12, Appl
21	34	100.0	34	8	US-10-762-915-1	Sequence 1, Appli
22	34	100.0	34	8	US-10-762-915-2	Sequence 2, Appli
23	34	100.0	34	8	US-10-762-915-3	Sequence 3, Appli
24	34	100.0	34	8	US-10-762-915-6	Sequence 6, Appli
25	34	100.0	34	8	US-10-762-915-7	Sequence 7, Appli
26	34	100.0	34	8	US-10-762-915-8	Sequence 8, Appli
27	34	100.0	34	8	US-10-762-915-21	Sequence 21, Appl
28	34	100.0	34	8	US-10-762-915-22	Sequence 22, Appl
29	34	100.0	34	8	US-10-762-915-27	Sequence 27, Appl
30	34	100.0	34	8	US-10-762-915-148	Sequence 148, App
31	34	100.0	34	8	US-10-812-642-93	Sequence 93, Appl
32	34	100.0	34	8	US-10-812-642-115	Sequence 115, App
33	34	100.0	34	8	US-10-812-642-121	Sequence 121, App
34	34	100.0	34	8	US-10-812-642-171	Sequence 171, App
35	34	100.0	34	8	US-10-812-642-172	Sequence 172, App
36	34	100.0	34	8	US-10-812-642-173	Sequence 173, App
37	34	100.0	34	8	US-10-812-642-174	Sequence 174, App
38	34	100.0	34	8	US-10-812-642-175	Sequence 175, App
39	34	100.0	34	8	US-10-812-642-176	Sequence 176, App
40	34	100.0	34	8	US-10-812-642-177	Sequence 177, App
41	34	100.0	34	8	US-10-812-642-178	Sequence 178, App
42	34	100.0	34	8	US-10-812-642-179	Sequence 179, App
43	34	100.0	34	8	US-10-812-642-180	Sequence 180, App
44	34	100.0	34	8	US-10-812-642-181	Sequence 181, App
45	34	100.0	34	8	US-10-812-642-182	Sequence 182, App

ALIGNMENTS

RESULT 1
US-09-791-301-93
; Sequence 93, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F.
US-09-791-301-93

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 2
US-09-791-301-115
; Sequence 115, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F.
US-09-791-301-115

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 3
US-09-791-301-121
; Sequence 121, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F.
US-09-791-301-121

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 4
US-09-791-301-171
; Sequence 171, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-171

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 5
US-09-791-301-172
; Sequence 172, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'OCH3;
;   OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-172

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 6
US-09-791-301-173
; Sequence 173, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-4 are 2'OCH3; linkage at positions 34 and 35 is
;   OTHER INFORMATION: 3'-3'.
US-09-791-301-173

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 7
US-09-791-301-174
; Sequence 174, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
```

```
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 5, 8, and 11 are 2'OCH3; linkage at positions 34
;   OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-174

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 8
US-09-791-301-175
; Sequence 175, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a' and g's at positions
;   OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
;   OTHER INFORMATION: is 3'-3'.
US-09-791-301-175

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 9
US-09-791-301-176
; Sequence 176, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 20, 22 and 24 are 2'-OCH3; linkage at positions 34
;   OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-176

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 10
US-09-791-301-177
; Sequence 177, Application US/09791301
; Publication No. US20030064943A1
```

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; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 25, 28 and 30 are 2'-OCH3; linkage at positions 34
;   OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-177

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 11
US-09-791-301-178
; Sequence 178, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; g at position 20 is
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-178

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 12
US-09-791-301-179
; Sequence 179, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a at position 22 is
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-179
```

```
  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 13
US-09-791-301-180
; Sequence 180, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a at position 24 is
;   OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-180

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 14
US-09-791-301-181
; Sequence 181, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Sequence
;   NAME/KEY: modified_base
;   LOCATION: (1)..(34)
;   OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
;   OTHER INFORMATION: 1-5, 8, 11, 25 and 30 are 2'-OCH3; linkage at
;   OTHER INFORMATION: positions 34 and 35 is 3'-3'.
US-09-791-301-181

  Query Match             100.0%;  Score 34;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 15
US-09-791-301-182
; Sequence 182, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
;  APPLICANT: Pagratis, Nikos
;  APPLICANT:  Lochrie, Michael
;  APPLICANT:  Gold, Larry
;  TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: NEX 87/C
;  CURRENT APPLICATION NUMBER: US/09/791,301
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/046,247
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 08/458,424
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 07/714,131
;  PRIOR FILING DATE: 1991-06-10
;  PRIOR APPLICATION NUMBER: 07/931,473
;  PRIOR FILING DATE: 1992-08-17
;  PRIOR APPLICATION NUMBER: 07/964,624
;  PRIOR FILING DATE: 1992-10-21
;  PRIOR APPLICATION NUMBER: 08/117,991
;  PRIOR FILING DATE: 1993-09-08
;  PRIOR APPLICATION NUMBER: 07/536,428
;  PRIOR FILING DATE: 1990-06-11
;  PRIOR APPLICATION NUMBER: 09/363,939
;  PRIOR FILING DATE: 1999-07-29
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; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
; OTHER INFORMATION: 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
; OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-182

Query Match 100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||
Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

Search completed: December 27, 2005, 16:59:16
Job time : 816 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 15:06:46 ; Search time 296 Seconds
(without alignments)
59.610 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguuauuacagagucuguauagcuguacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20.2	59.4	150481	7	US-11-112-908-37	Sequence 37, Appl
c	2	20.2	59.4	171162	7	US-11-112-908-38	Sequence 38, Appl
	3	19.2	56.5	691	6	US-10-750-185-64880	Sequence 64880, A
c	4	19.2	56.5	2279	6	US-10-750-185-57144	Sequence 57144, A
c	5	18.6	54.7	971	6	US-10-750-185-62416	Sequence 62416, A
	6	18.6	54.7	1527	6	US-10-750-185-33471	Sequence 33471, A
c	7	18.4	54.1	1086	6	US-10-750-185-51403	Sequence 51403, A
c	8	18.2	53.5	25	7	US-11-121-849-617034	Sequence 617034,
	9	18.2	53.5	435	6	US-10-467-657-263	Sequence 263, App
	10	18.2	53.5	435	6	US-10-467-657-3599	Sequence 3599, Ap
c	11	18.2	53.5	1671	6	US-10-750-185-56074	Sequence 56074, A
	12	18.2	53.5	1894	6	US-10-995-561-248	Sequence 248, App
	13	18.2	53.5	2439	6	US-10-995-561-249	Sequence 249, App
	14	18.2	53.5	2789	6	US-10-995-561-250	Sequence 250, App
c	15	18.2	53.5	20991	6	US-10-995-561-13488	Sequence 13488, A
c	16	18.2	53.5	31657	6	US-10-995-561-13334	Sequence 13334, A
	17	18.2	53.5	33175	6	US-10-995-561-13270	Sequence 13270, A
c	18	18	52.9	5134	7	US-11-060-005-1	Sequence 1, Appli
c	19	18	52.9	6160	7	US-11-060-005-3	Sequence 3, Appli
	20	18	52.9	148220	7	US-11-121-086-90	Sequence 90, Appl
c	21	18	52.9	207600	7	US-11-112-908-31	Sequence 31, Appl
	22	17.8	52.4	201	6	US-10-995-561-53373	Sequence 53373, A
c	23	17.8	52.4	201	6	US-10-995-561-74017	Sequence 74017, A
	24	17.8	52.4	598	6	US-10-750-185-769	Sequence 769, App
c	25	17.8	52.4	819	6	US-10-793-626-3197	Sequence 3197, Ap
c	26	17.8	52.4	3244	6	US-10-793-626-3567	Sequence 3567, Ap
c	27	17.8	52.4	13395	6	US-10-995-561-13452	Sequence 13452, A
	28	17.8	52.4	35101	6	US-10-995-561-13315	Sequence 13315, A
c	29	17.6	51.8	367	8	US-11-132-285-57	Sequence 57, Appl
c	30	17.6	51.8	1000	6	US-10-750-185-26175	Sequence 26175, A
	31	17.6	51.8	1081	6	US-10-750-185-54369	Sequence 54369, A
c	32	17.6	51.8	1322	6	US-10-750-185-41390	Sequence 41390, A
	33	17.6	51.8	2203	6	US-10-750-185-36421	Sequence 36421, A
	34	17.6	51.8	179777	7	US-11-121-086-106	Sequence 106, App
c	35	17.4	51.2	1087	6	US-10-750-185-42060	Sequence 42060, A
c	36	17.4	51.2	1485	6	US-10-750-185-41900	Sequence 41900, A
c	37	17.4	51.2	1524	6	US-10-750-185-42660	Sequence 42660, A
c	38	17.4	51.2	2482	6	US-10-750-185-42895	Sequence 42895, A
c	39	17.4	51.2	2926	6	US-10-750-185-48539	Sequence 48539, A
	40	17.4	51.2	2987	6	US-10-793-626-4367	Sequence 4367, Ap
c	41	17.4	51.2	3137	6	US-10-793-626-3842	Sequence 3842, Ap
c	42	17.4	51.2	3569	6	US-10-793-626-4443	Sequence 4443, Ap
c	43	17.4	51.2	4297	6	US-10-793-626-4092	Sequence 4092, Ap
c	44	17.4	51.2	150314	7	US-11-112-908-24	Sequence 24, Appl
c	45	17.4	51.2	156544	7	US-11-121-086-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-11-112-908-37/c
; Sequence 37, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 150481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-37

Query Match 59.4%; Score 20.2; DB 7; Length 150481;
Best Local Similarity 48.5%; Pred. No. 14;
Matches 16; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUC 33
              | | |:  ::||||||:|: :|:|||  :| :|
Db      67191 GTAAGTATTTACAGAGTCTTTATAGCATTAGTC 67159
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RESULT 2
US-11-112-908-38/c
; Sequence 38, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908

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;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
;   LENGTH: 171162
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-38

  Query Match            59.4%;  Score 20.2;  DB 7;  Length 171162;
  Best Local Similarity   48.5%;  Pred. No. 14;
  Matches   16;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUC 33
              | | |:  ::||||||:|: :|:|||  :| :|
Db     139691 GTAAGTATTTACAGAGTCTTTATAGCATTAGTC 139659


RESULT 3
US-10-750-185-64880
; Sequence 64880, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 64880
;   LENGTH: 691
;   TYPE: DNA
;   ORGANISM: Bovine  19866881409947
US-10-750-185-64880

  Query Match            56.5%;  Score 19.2;  DB 6;  Length 691;
  Best Local Similarity   50.0%;  Pred. No. 13;
  Matches   12;  Conservative    9;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 UUAUUACAGAGUCUGUAUAGCUGU 29
              : |::|||| |:|:|:|:|| :|:
Db        450 TCATTACAGGGTCTGTATAGTTGT 473


RESULT 4
US-10-750-185-57144/c
; Sequence 57144, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 57144
;   LENGTH: 2279
;   TYPE: DNA
;   ORGANISM: Bovine  19866880808150
US-10-750-185-57144

  Query Match            56.5%;  Score 19.2;  DB 6;  Length 2279;
  Best Local Similarity   50.0%;  Pred. No. 17;
  Matches   16;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACU 32
              || | ::| : |||||:|:| |: ||:|  |:
Db        125 GGTGTTTACTGCAGAGTCTGAATTGCTGCCCT 94


RESULT 5
US-10-750-185-62416/c
; Sequence 62416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 62416
;   LENGTH: 971
;   TYPE: DNA
;   ORGANISM: Bovine  19866880400331
US-10-750-185-62416

  Query Match            54.7%;  Score 18.6;  DB 6;  Length 971;
  Best Local Similarity   56.0%;  Pred. No. 26;
  Matches   14;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         10 UACAGAGUCUGUAUAGCUGUACUCC 34
              :||||||:| |: :|||:|:| : |
Db        173 TACAGAGTCAGTTTAGCTGTAGTAC 149


RESULT 6
US-10-750-185-33471
; Sequence 33471, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
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;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33471
;   LENGTH: 1527
;   TYPE: DNA
;   ORGANISM: Bovine  19866882040664
US-10-750-185-33471

  Query Match            54.7%;  Score 18.6;  DB 6;  Length 1527;
  Best Local Similarity  45.5%;  Pred. No. 29;
  Matches   15;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUC 33
              |||  ::  :|||| :|: :|:| |:| ||:|
Db        299 GGACTTTTCTACAGCTTCTTTATACCTGAACTC 331


RESULT 7
US-10-750-185-51403/c
; Sequence 51403, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51403
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Bovine  19866880936749
US-10-750-185-51403

  Query Match            54.1%;  Score 18.4;  DB 6;  Length 1086;
  Best Local Similarity  57.1%;  Pred. No. 33;
  Matches   16;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUG 28
              ||||  : ::|||||:| | |: ||:|
Db       1042 GGAGCATGTTACAGAGTCAGGATTGCTG 1015


RESULT 8
US-11-121-849-617034/c
; Sequence 617034, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 617034
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-617034

  Query Match            53.5%;  Score 18.2;  DB 7;  Length 25;
  Best Local Similarity  56.5%;  Pred. No. 19;
  Matches   13;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 UUACAGAGUCUGUAUAGCUGUAC 31
              ::| ||||: :| |:|||:|:||
Db         24 TTAGAGAGTGTGCATAGCTGTAC 2


RESULT 9
US-10-467-657-263
; Sequence 263, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 263
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-263

  Query Match            53.5%;  Score 18.2;  DB 6;  Length 435;
  Best Local Similarity  48.4%;  Pred. No. 34;
  Matches   15;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 GGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              | ::|: | ||| : :| | | |:|:||:||
Db        402 GATTATCAAAGACTATGAAGAACTGTACTCC 432


RESULT 10
US-10-467-657-3599
; Sequence 3599, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3599
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3599

  Query Match            53.5%;  Score 18.2;  DB 6;  Length 435;
  Best Local Similarity  48.4%;  Pred. No. 34;
  Matches   15;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;
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Qy          4 GGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              | ::|: | ||| : :| | | |:|:||:||
Db        402 GATTATCAAAGACTATGAAGAACTGTACTCC 432


RESULT 11
US-10-750-185-56074/c
; Sequence 56074, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 56074
;   LENGTH: 1671
;   TYPE: DNA
;   ORGANISM: Bovine  19866881576202
US-10-750-185-56074

  Query Match             53.5%;  Score 18.2;  DB 6;  Length 1671;
  Best Local Similarity   60.9%;  Pred. No. 44;
  Matches   14;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAU 23
              |||||::|::|||||  |:| |:
Db        365 GGAGGTTATTACAGATACTGAAT 343


RESULT 12
US-10-995-561-248
; Sequence 248, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 248
;   LENGTH: 1894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-248

  Query Match             53.5%;  Score 18.2;  DB 6;  Length 1894;
  Best Local Similarity   58.1%;  Pred. No. 45;
  Matches   18;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUAC 31
              || ||: |::|||||  |:| | | |:| ||
Db        169 GGTGGTCATTACAGACCCTGAAAAACTGGAC 199


RESULT 13
US-10-995-561-249
; Sequence 249, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 249
;   LENGTH: 2439
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-249

  Query Match             53.5%;  Score 18.2;  DB 6;  Length 2439;
  Best Local Similarity   58.1%;  Pred. No. 48;
  Matches   18;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUAC 31
              || ||: |::|||||  |:| | | |:| ||
Db        974 GGTGGTCATTACAGACCCTGAAAAACTGGAC 1004


RESULT 14
US-10-995-561-250
; Sequence 250, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 250
;   LENGTH: 2789
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-250

  Query Match             53.5%;  Score 18.2;  DB 6;  Length 2789;
  Best Local Similarity   58.1%;  Pred. No. 49;
  Matches   18;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUAC 31
              || ||: |::|||||  |:| | | |:| ||
Db        974 GGTGGTCATTACAGACCCTGAAAAACTGGAC 1004


RESULT 15
US-10-995-561-13488/c
; Sequence 13488, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13488
;   LENGTH: 20991
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13488
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Query Match 53.5%; Score 18.2; DB 6; Length 20991;
Best Local Similarity 58.1%; Pred. No. 75;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUAC 31
              || ||: |::||||| |:| | | |:| ||
Db         77 GGTGGTCATTACAGACCCTGAAAAACTGGAC 47
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Search completed: December 27, 2005, 17:04:24
Job time : 297 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 13:28:20 ; Search time 1988 Seconds
(without alignments)
972.172 Million cell updates/sec

Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguuauuacagagucuguauagcuguacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	34	6	AR193289	AR193289 Sequence
2	34	100.0	34	6	AR193311	AR193311 Sequence
3	34	100.0	34	6	AR193317	AR193317 Sequence
4	34	100.0	34	6	AR193361	AR193361 Sequence
5	34	100.0	34	6	AR193362	AR193362 Sequence
6	34	100.0	34	6	AR193363	AR193363 Sequence
7	34	100.0	34	6	AR193364	AR193364 Sequence
8	34	100.0	34	6	AR193365	AR193365 Sequence
9	34	100.0	34	6	AR193366	AR193366 Sequence
10	34	100.0	34	6	AR193367	AR193367 Sequence
11	34	100.0	34	6	AR193368	AR193368 Sequence
12	34	100.0	34	6	AR193369	AR193369 Sequence
13	34	100.0	34	6	AR193370	AR193370 Sequence
14	34	100.0	34	6	AR193371	AR193371 Sequence
15	34	100.0	34	6	AR193372	AR193372 Sequence
16	34	100.0	34	6	AR193373	AR193373 Sequence
17	34	100.0	34	6	AR193374	AR193374 Sequence
18	34	100.0	34	6	AR193375	AR193375 Sequence
19	34	100.0	34	6	AR193376	AR193376 Sequence
20	34	100.0	34	6	AR491289	AR491289 Sequence
21	34	100.0	34	6	AR491311	AR491311 Sequence
22	34	100.0	34	6	AR491317	AR491317 Sequence
23	34	100.0	34	6	AR491361	AR491361 Sequence
24	34	100.0	34	6	AR491362	AR491362 Sequence
25	34	100.0	34	6	AR491363	AR491363 Sequence
26	34	100.0	34	6	AR491364	AR491364 Sequence
27	34	100.0	34	6	AR491365	AR491365 Sequence
28	34	100.0	34	6	AR491366	AR491366 Sequence
29	34	100.0	34	6	AR491367	AR491367 Sequence
30	34	100.0	34	6	AR491368	AR491368 Sequence
31	34	100.0	34	6	AR491369	AR491369 Sequence
32	34	100.0	34	6	AR491370	AR491370 Sequence
33	34	100.0	34	6	AR491371	AR491371 Sequence
34	34	100.0	34	6	AR491372	AR491372 Sequence
35	34	100.0	34	6	AR491373	AR491373 Sequence
36	34	100.0	34	6	AR491374	AR491374 Sequence
37	34	100.0	34	6	AR491375	AR491375 Sequence
38	34	100.0	34	6	AR491376	AR491376 Sequence
39	34	100.0	36	6	AR193288	AR193288 Sequence
40	34	100.0	36	6	AR193310	AR193310 Sequence
41	34	100.0	36	6	AR491288	AR491288 Sequence
42	34	100.0	36	6	AR491310	AR491310 Sequence
43	34	100.0	37	6	AR193312	AR193312 Sequence
44	34	100.0	37	6	AR491312	AR491312 Sequence
45	34	100.0	43	6	AR193287	AR193287 Sequence

ALIGNMENTS

RESULT 1
AR193289
LOCUS AR193289 34 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 93 from patent US 6346611.
ACCESSION AR193289
VERSION AR193289.1 GI:20239254
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Pagratis,N., Lochrie,M. and Gold,L.
TITLE High affinity TGf.beta. nucleic acid ligands and inhibitors
JOURNAL Patent: US 6346611-A 93 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 67.6%; Pred. No. 0.00024;
Matches 23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||::|::||||||:|:|:|:|||:|:||:||
Db 1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34

RESULT 2
AR193311
LOCUS AR193311 34 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 115 from patent US 6346611.
ACCESSION AR193311
VERSION AR193311.1 GI:20239276
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Pagratis,N., Lochrie,M. and Gold,L.

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  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 115 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::|||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 3
AR193317
LOCUS       AR193317                  34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 121 from patent US 6346611.
ACCESSION   AR193317
VERSION     AR193317.1  GI:20239282
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 121 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::|||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 4
AR193361
LOCUS       AR193361                  34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 171 from patent US 6346611.
ACCESSION   AR193361
VERSION     AR193361.1  GI:20239326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 171 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::|||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 5
AR193362
LOCUS       AR193362                  34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 172 from patent US 6346611.
ACCESSION   AR193362
VERSION     AR193362.1  GI:20239327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 172 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::|||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 6
AR193363
LOCUS       AR193363                  34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 173 from patent US 6346611.
ACCESSION   AR193363
VERSION     AR193363.1  GI:20239328
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 173 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::|||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 7
AR193364
LOCUS       AR193364                  34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 174 from patent US 6346611.
ACCESSION   AR193364
VERSION     AR193364.1  GI:20239329
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
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```
  JOURNAL   Patent: US 6346611-A 174 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 8
AR193365
LOCUS       AR193365                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 175 from patent US 6346611.
ACCESSION   AR193365
VERSION     AR193365.1  GI:20239330
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 175 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 9
AR193366
LOCUS       AR193366                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 176 from patent US 6346611.
ACCESSION   AR193366
VERSION     AR193366.1  GI:20239331
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 176 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 10
AR193367
LOCUS       AR193367                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 177 from patent US 6346611.
ACCESSION   AR193367
VERSION     AR193367.1  GI:20239332
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 177 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 11
AR193368
LOCUS       AR193368                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 178 from patent US 6346611.
ACCESSION   AR193368
VERSION     AR193368.1  GI:20239333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 178 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 12
AR193369
LOCUS       AR193369                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 179 from patent US 6346611.
ACCESSION   AR193369
VERSION     AR193369.1  GI:20239334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 179 12-FEB-2002;
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FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              |||||::|::||||||:|:|:|:|||:|:||:||
Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 13
AR193370
LOCUS       AR193370                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 180 from patent US 6346611.
ACCESSION   AR193370
VERSION     AR193370.1  GI:20239335
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 180 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
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ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 14
AR193371
LOCUS       AR193371                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 181 from patent US 6346611.
ACCESSION   AR193371
VERSION     AR193371.1  GI:20239336
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 181 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


RESULT 15
AR193372
LOCUS       AR193372                34 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 182 from patent US 6346611.
ACCESSION   AR193372
VERSION     AR193372.1  GI:20239337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Pagratis,N., Lochrie,M. and Gold,L.
  TITLE     High affinity TGf.beta. nucleic acid ligands and inhibitors
  JOURNAL   Patent: US 6346611-A 182 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .34
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   67.6%;  Pred. No. 0.00024;
  Matches   23;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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Db          1 GGAGGTTATTACAGAGTCTGTATAGCTGTACTCC 34


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Job time : 1988 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 12:44:50 ; Search time 487 Seconds
(without alignments)
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Title: US-10-812-642-115
Perfect score: 34
Sequence: 1 ggagguuauuacagagucuguauagcuguacucc 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	34	5	AAF90818	Aaf90818 TGFbeta2
2	34	100.0	34	5	AAF90873	Aaf90873 NX22284 l
3	34	100.0	34	5	AAF90877	Aaf90877 NX22284 l
4	34	100.0	34	5	AAF90796	Aaf90796 TGFbeta2
5	34	100.0	34	5	AAF90870	Aaf90870 NX22284 l
6	34	100.0	34	5	AAF90883	Aaf90883 NX22284 l
7	34	100.0	34	5	AAF90824	Aaf90824 TGFbeta2
8	34	100.0	34	5	AAF90869	Aaf90869 NX22284 l
9	34	100.0	34	5	AAF90871	Aaf90871 NX22284 l
10	34	100.0	34	5	AAF90872	Aaf90872 NX22284 l
11	34	100.0	34	5	AAF90879	Aaf90879 NX22284 l
12	34	100.0	34	5	AAF90882	Aaf90882 NX22284 l
13	34	100.0	34	5	AAF90868	Aaf90868 NX22284 l
14	34	100.0	34	5	AAF90876	Aaf90876 NX22284 l
15	34	100.0	34	5	AAF90875	Aaf90875 NX22284 l
16	34	100.0	34	5	AAF90881	Aaf90881 NX22284 l
17	34	100.0	34	5	AAF90878	Aaf90878 NX22284 l
18	34	100.0	34	5	AAF90874	Aaf90874 NX22284 l
19	34	100.0	34	5	AAF90880	Aaf90880 NX22284 l
20	34	100.0	34	12	ADO59385	Ado59385 TGF-beta-
21	34	100.0	34	12	ADO59391	Ado59391 Monodenta
22	34	100.0	34	13	ADQ89377	Adq89377 Human TGF
23	34	100.0	34	13	ADQ89381	Adq89381 Human TGF
24	34	100.0	34	13	ADQ89390	Adq89390 Human TGF
25	34	100.0	34	13	ADQ89376	Adq89376 Human TGF
26	34	100.0	34	13	ADQ89383	Adq89383 Human TGF
27	34	100.0	34	13	ADQ89378	Adq89378 Human TGF
28	34	100.0	34	13	ADQ89382	Adq89382 Human TGF
29	34	100.0	34	13	ADQ89510	Adq89510 Human TGF
30	34	100.0	34	13	ADQ89520	Adq89520 Human TGF
31	34	100.0	34	14	AEA28125	Aea28125 TGFbeta2-
32	34	100.0	36	5	AAF90795	Aaf90795 TGFbeta2
33	34	100.0	36	5	AAF90817	Aaf90817 TGFbeta2
34	34	100.0	37	5	AAF90819	Aaf90819 TGFbeta2
35	34	100.0	43	5	AAF90794	Aaf90794 TGFbeta2
36	34	100.0	56	5	AAF90793	Aaf90793 TGFbeta2
37	34	100.0	57	5	AAF90792	Aaf90792 TGFbeta2
38	34	100.0	65	13	ADQ89454	Adq89454 Human TGF
39	34	100.0	70	5	AAF90790	Aaf90790 TGFbeta2
c 40	34	100.0	82	13	ADQ89398	Adq89398 Human TGF
41	33	97.1	33	5	AAF90802	Aaf90802 TGFbeta2
42	33	97.1	33	5	AAF90821	Aaf90821 TGFbeta2
43	33	97.1	65	5	AAF90864	Aaf90864 Oligonucl
44	32.4	95.3	70	5	AAF90791	Aaf90791 TGFbeta2
45	32	94.1	32	5	AAF90822	Aaf90822 TGFbeta2

ALIGNMENTS

RESULT 1
AAF90818
ID AAF90818 standard; RNA; 34 BP.
XX
AC AAF90818;
XX
DT 03-MAY-2001 (first entry)
XX
DE TGFbeta2 ligand 21a-21 truncate #28.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 70; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention

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XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 2
AAF90873
ID   AAF90873 standard; RNA; 34 BP.
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AC   AAF90873;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #6.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 3
AAF90877
ID   AAF90877 standard; RNA; 34 BP.
XX
AC   AAF90877;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #10.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 34;
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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 4
AAF90796
ID   AAF90796 standard; RNA; 34 BP.
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AC   AAF90796;
XX
DT   03-MAY-2001  (first entry)
XX
DE   TGFbeta2 ligand 21a-21 truncate #6.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
```

```
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 68; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 5
AAF90870
ID   AAF90870 standard; RNA; 34 BP.
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AC   AAF90870;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #3.
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KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
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OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


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XX
AC   AAF90883;
XX
DT   03-MAY-2001  (first entry)
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KW   systemic evolution of ligands by exponential enrichment; ss.
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OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
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  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 7
AAF90824
ID   AAF90824 standard; RNA; 34 BP.
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AC   AAF90824;
XX
DT   03-MAY-2001  (first entry)
XX
DE   TGFbeta2 ligand 21a-21 truncate #34.
XX
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KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 70; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
||||||||||||||||||||||||||||||||||
Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 8
AAF90869
ID AAF90869 standard; RNA; 34 BP.
XX
AC AAF90869;
XX
DT 03-MAY-2001 (first entry)
XX
DE NX22284 ligand variant #2.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 78; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 9
AAF90871
ID AAF90871 standard; RNA; 34 BP.
XX
AC AAF90871;
XX
DT 03-MAY-2001 (first entry)
XX
DE NX22284 ligand variant #4.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 78; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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RESULT 10
AAF90872
ID AAF90872 standard; RNA; 34 BP.
XX
AC AAF90872;
XX
DT 03-MAY-2001 (first entry)
XX
DE NX22284 ligand variant #5.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 78; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

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  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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RESULT 11
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ID AAF90879 standard; RNA; 34 BP.
XX
AC AAF90879;
XX
DT 03-MAY-2001 (first entry)
XX
DE NX22284 ligand variant #12.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 78; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

```
  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
```

RESULT 12
AAF90882
ID AAF90882 standard; RNA; 34 BP.
XX
AC AAF90882;
XX
DT 03-MAY-2001 (first entry)
XX
DE NX22284 ligand variant #15.
XX
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW systemic evolution of ligands by exponential enrichment; ss.
XX
OS Homo sapiens.
XX
PN WO200109156-A1.
XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX

```
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 13
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ID   AAF90868 standard; RNA; 34 BP.
XX
AC   AAF90868;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #1.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 14
AAF90876
ID   AAF90876 standard; RNA; 34 BP.
XX
AC   AAF90876;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #9.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020397.
XX
PR   29-JUL-1999;   99US-00363939.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Lochrie M,  Gold L;
XX
DR   WPI; 2001-218217/22.
XX
PT   New RNA ligand to human transforming growth factor beta2, useful as
PT   pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS   Claim 1; Page 78; 178pp; English.
XX
CC   The present invention relates to non-naturally occurring, high-affinity
CC   RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC   oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC   for Systemic Evolution of Ligands by EXponential Enrichment). The
CC   oligonucleotide ligands are useful in any process in which binding to
CC   TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC   diagnostics, imaging agents and immunohistochemical reagents. The present
CC   sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||
Db          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34


RESULT 15
AAF90875
ID   AAF90875 standard; RNA; 34 BP.
XX
AC   AAF90875;
XX
DT   03-MAY-2001  (first entry)
XX
DE   NX22284 ligand variant #8.
XX
KW   Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW   systemic evolution of ligands by exponential enrichment; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109156-A1.
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XX
PD 08-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US020397.
XX
PR 29-JUL-1999; 99US-00363939.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Pagratis N, Lochrie M, Gold L;
XX
DR WPI; 2001-218217/22.
XX
PT New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immnohistochemical reagents.
XX
PS Claim 1; Page 78; 178pp; English.
XX
CC The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systemic Evolution of Ligands by EXponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents. The present
CC sequence is an oligonucleotide used in the present invention
XX
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
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Db 1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34

Search completed: December 27, 2005, 15:06:36
Job time : 487 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:30:56 ; Search time 3758 Seconds
(without alignments)
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Title: US-10-812-642-115
Perfect score: 34
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	22.2	65.3	732	7	CR420095	CR420095 CR420095
c	2	21.8	64.1	483	9	AQ146760	AQ146760 HS_2241_B
c	3	21.4	62.9	329	7	CR469204	CR469204 CR469204
	4	21.4	62.9	730	8	CX909337	CX909337 JGI_CAAN1
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	6	21.4	62.9	772	5	BU415821	BU415821 603669377
	7	21.4	62.9	1209	10	CL043735	CL043735 CH216-58O
c	8	21.2	62.4	508	9	AQ788713	AQ788713 HS_5549_A
c	9	21.2	62.4	734	9	BZ055939	BZ055939 11f26d01.
	10	21.2	62.4	900	10	DU036738	DU036738 19377 Tom
	11	21.2	62.4	1163	8	DN704358	DN704358 CLJ52-H09
	12	21	61.8	533	9	BZ680408	BZ680408 PUBGI05TD
	13	21	61.8	632	10	CZ836446	CZ836446 OC__Ba021
	14	21	61.8	679	11	CR157585	CR157585 Forward s
	15	21	61.8	728	9	AQ258623	AQ258623 nbxb0020N
	16	21	61.8	977	9	BZ394307	BZ394307 EINCM21TR
c	17	20.8	61.2	251	1	AV274404	AV274404 AV274404
	18	20.8	61.2	281	5	BX635814	BX635814 BX635814
c	19	20.8	61.2	288	1	AA645178	AA645178 vs79a05.r
c	20	20.8	61.2	319	8	CX200320	CX200320 MNS01050
	21	20.8	61.2	334	3	BM940310	BM940310 UI-M-CG0p
	22	20.8	61.2	381	9	AQ567614	AQ567614 HS_2118_B
	23	20.8	61.2	399	1	AI594558	AI594558 vo06g05.y
	24	20.8	61.2	437	2	BE986100	BE986100 UI-M-CG0p
c	25	20.8	61.2	476	3	BM941736	BM941736 UI-M-CG0p
c	26	20.8	61.2	480	1	AI592407	AI592407 vs79a05.y
	27	20.8	61.2	497	1	AA606330	AA606330 vo06g05.r
c	28	20.8	61.2	529	1	AA980547	AA980547 ua42f01.r
	29	20.8	61.2	543	2	BG946683	BG946683 949013D09
c	30	20.8	61.2	549	6	CA392086	CA392086 cs21e09.y
c	31	20.8	61.2	560	5	BX641668	BX641668 DKFZp686J
c	32	20.8	61.2	565	2	BE290104	BE290104 601089086
c	33	20.8	61.2	592	3	BI730042	BI730042 603349653
c	34	20.8	61.2	600	5	BU918118	BU918118 5013-60 M
c	35	20.8	61.2	600	5	BU918131	BU918131 5013-76 M
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	37	20.8	61.2	653	9	AZ010030	AZ010030 RPCI-23-2
	38	20.8	61.2	691	7	CR589375	CR589375 CR589375
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c	41	20.8	61.2	755	8	CX210472	CX210472 MNS29414
c	42	20.8	61.2	767	2	BF169054	BF169054 601773331
c	43	20.8	61.2	791	6	CB952424	CB952424 AGENCOURT
c	44	20.8	61.2	848	7	CK847093	CK847093 969680 MA
c	45	20.8	61.2	1482	4	AK079249	AK079249 Mus muscu

ALIGNMENTS

RESULT 1
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LOCUS CR420095 732 bp mRNA linear EST 17-JUN-2004
DEFINITION CR420095 XGC-tailbud Xenopus tropicalis cDNA clone TTbA067g23 5', mRNA sequence.
ACCESSION CR420095
VERSION CR420095.1 GI:48913503
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 732)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTbA067g23.p1kSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
Seq primer: SP6.
FEATURES Location/Qualifiers
source 1. .732
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/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTbA067g23"
/dev_stage="tailbud (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

Query Match 65.3%; Score 22.2; DB 7; Length 732;
Best Local Similarity 51.9%; Pred. No. 1.6e+02;
Matches 14; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
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LOCUS       AQ146760                483 bp    DNA     linear   GSS 08-OCT-1998
DEFINITION  HS_2241_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2241 Col=6 Row=H, genomic survey
            sequence.
ACCESSION   AQ146760
VERSION     AQ146760.1  GI:3537413
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2241  row: H  column: 6
            Class: BAC ends
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   14;  Conservative    9;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GUUAUUACAGAGUCUGUAUAGCUGU 29
              |: |::|||||:|:|:|:|| :|:
Db        193 GTCATTACAGAGTCTGTATAGTTGT 169


RESULT 3
CR469204/c
LOCUS       CR469204                329 bp    mRNA    linear   EST 01-JUL-2004
DEFINITION  CR469204 Rat pBluescript Lion Rattus norvegicus cDNA clone
            LIONp463E08404 3', mRNA sequence.
ACCESSION   CR469204
VERSION     CR469204.1  GI:49601553
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schlueter,T.,
            Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Rat ArrayTAG cDNA
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; LIONp463E08404.
            RZPDLIB;
            Rat ArrayTAG cDNA
            http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=463 Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            RP: CAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="LIONp463E08404"
                     /lab_host="DH10B"
                     /clone_lib="Rat pBluescript Lion"
ORIGIN

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  Best Local Similarity   58.1%;  Pred. No. 3.2e+02;
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RESULT 4
CX909337
LOCUS       CX909337                730 bp    mRNA    linear   EST 04-AUG-2005
DEFINITION  JGI_CAAN1789.rev NIH_XGC_tropTe4 Xenopus tropicalis cDNA clone
            IMAGE:7687386 3', mRNA sequence.
ACCESSION   CX909337
VERSION     CX909337.2  GI:71830453
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 730)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     On Feb 4, 2005 this sequence version replaced gi:58648681.
            Other_ESTs: JGI_CAAN1789.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
            University of California, Berkeley:
            http://tropicalis.berkeley.edu/home)
            cDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
```

Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAN 0017 row: i column: 16
High quality sequence stop: 725
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .730
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7687386"
/sex="male"
/tissue_type="Testes"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B"
/clone_lib="NIH_XGC_tropTe4"
/note="Vector: pCMVsport6; Site_1: SalI; Site_2: NotI; This library was made from dT primed cDNA and cloned into Invitrogen pCMVsport6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCTAGATCGCGAG CGGCCGCCCTTTTTTTTTTTTTT 3'. CDNA were ligated to SalI adapter (5' TCGACCCACGCGTCCG and 5'CGGACGCGTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVsport6 vector."

ORIGIN

Query Match 62.9%; Score 21.4; DB 8; Length 730;
Best Local Similarity 45.2%; Pred. No. 3.6e+02;
Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GAGGUUAUUACAGAGUCUGUAUAGCUGUACU 32
|| |::|:: ||| |:|:|: :|| :|:| :
Db 255 GATGTTATTTCAGTGTCTGTTTAGATGTATT 285

RESULT 5
BU747611/c
LOCUS BU747611 769 bp mRNA linear EST 10-OCT-2002
DEFINITION CH3#014_B02T7 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#014_B02 5', mRNA sequence.
ACCESSION BU747611
VERSION BU747611.1 GI:23698691
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 769)
AUTHORS Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
TITLE Expressed sequence tags from Canine heart
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: CH3#014_B02T3
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Seq primer: T7: TAATACGACTCACTATAGGG
High quality sequence start: 176
High quality sequence stop: 435.

FEATURES Location/Qualifiers
source 1. .769
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#014_B02"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"
/clone_lib="Canine heart normalized cDNA Library in pBluescript"
/note="Organ: heart; Vector: pBluescript; Site_1: 5' of vector NotI; Site_2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"

ORIGIN

Query Match 62.9%; Score 21.4; DB 5; Length 769;
Best Local Similarity 45.2%; Pred. No. 3.6e+02;
Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 3 AGGUUAUUACAGAGUCUGUAUAGCUGUACUC 33
|||::|:: | | : :|:|:|||:|: |:|
Db 689 AGGTTATTCTACACTGTGTATAGCTGTGCTC 659

RESULT 6
BU415821
LOCUS BU415821 772 bp mRNA linear EST 29-NOV-2002
DEFINITION 603669377F1 CSEQRBL06 Gallus gallus cDNA clone ChEST611i19 5', mRNA sequence.
ACCESSION BU415821
VERSION BU415821.1 GI:25908492
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 772)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES Location/Qualifiers
source 1. .772
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="ChEST611i19"
/sex="Male and female"
/tissue_type="Abdominal fat pad"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBL06"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagccccggatccgaaaaaaag] [5'aattcttttttttcggatccggggctgcacgc]"

```
ORIGIN

  Query Match            62.9%;  Score 21.4;  DB 5;  Length 772;
  Best Local Similarity   45.2%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 GGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||:: ::| || |:|:|:|:| |:|:  :||
Db        685 GGTTTTTATAGTGTCTGTATATCTGTGATCC 715


RESULT 7
CL043735
LOCUS       CL043735               1209 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-58O8_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-58O8,
            genomic survey sequence.
ACCESSION   CL043735
VERSION     CL043735.1  GI:40499648
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: Sp6 ATTTAGGTGACACTATAG
            Class: BAC ends
            High quality sequence start: 19
            High quality sequence stop: 631.
FEATURES             Location/Qualifiers
     source          1. .1209
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-58O8"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match            62.9%;  Score 21.4;  DB 10;  Length 1209;
  Best Local Similarity   45.2%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 GAGGUUAUUACAGAGUCUGUAUAGCUGUACU 32
              || |::|:: ||| |:|:|: :|| :|:| :
Db        285 GATGTTATTTCAGTGTCTGTTTAGATGTATT 315


RESULT 8
AQ788713/c
LOCUS       AQ788713               508 bp    DNA     linear   GSS 03-AUG-1999
DEFINITION  HS_5549_A1_H02_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1125 Col=3 Row=O, genomic survey sequence.
ACCESSION   AQ788713
VERSION     AQ788713.1  GI:5696337
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1125  row: O  column: 3
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 508.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=1125 Col=3 Row=O"
                     /sex="male"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match            62.4%;  Score 21.2;  DB 9;  Length 508;
  Best Local Similarity   61.5%;  Pred. No. 4.1e+02;
  Matches   16;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 AGGUUAUUACAGAGUCUGUAUAGCUG 28
              ||  :|::||||||:|:|:|:||| |
Db        471 AGTGTATTACAGAGTCTGTATAGCAG 446


RESULT 9
BZ055939/c
LOCUS       BZ055939               734 bp    DNA     linear   GSS 09-OCT-2002
DEFINITION  l1f26d01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ055939
VERSION     BZ055939.1  GI:23660972
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: l1f26  row: d  column: 01
```

```
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 47
            High quality sequence stop: 199.
FEATURES              Location/Qualifiers
     source           1. .734
                      /organism="Brassica oleracea"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:3712"
                      /clone_lib="B.oleracea002"
                      /note="Vector: pOTw13; Whole genome shotgun library from
                      flowering buds. DNA was purified  from a crude nuclear
                      prep using Brassica oleracea TO1000DH3 buds  provided by
                      Thosmas Osborn at the University of Wisconsin. Genomic
                      DNA was provided by Pablo Rabinowicz (CSHL) and the
                      shotgun library  prepared at Washington University Genome
                      Sequencing Center."
ORIGIN

  Query Match             62.4%;  Score 21.2;  DB 9;  Length 734;
  Best Local Similarity   55.9%;  Pred. No. 4.4e+02;
  Matches   19;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              | || : |::|| |||: :| | |||:| ||:||
Db        250 GTAGATGATTACCGAGTGTGGAGAGCTGCACTCC 217


RESULT 10
DU036738
LOCUS       DU036738                900 bp    DNA     linear   GSS 12-AUG-2005
DEFINITION  19377 Tomato HindIII BAC Library Lycopersicon esculentum genomic
            clone LE_HBa0078L17 5, genomic survey sequence.
ACCESSION   DU036738
VERSION     DU036738.1  GI:72454464
KEYWORDS    GSS.
SOURCE      Lycopersicon esculentum (Solanum lycopersicum)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Mueller,L.A., Buels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J.,
            Van Eck,J. and Stack,S.
  TITLE     BAC end sequencing from three Solanum lycopersicon libraries
  JOURNAL   Unpublished (2005)
COMMENT     Other_GSSs: 19376
            Contact: Lukas Mueller
            Tanksley Lab, Dept. of Plant Breeding
            Cornell University
            251 Emerson Hall, Ithaca, NY 14853, USA
            Tel: 607-255-6557
            Fax: 607-255-6683
            Email: sgn-feedback@sgn.cornell.edu
            Insert Length: 84895   Std Error: 0.00
            Plate: 78  row: L  column: 17
            Seq primer: T7
            Class: BAC ends
            High quality sequence start: 49
            High quality sequence stop: 735.
FEATURES              Location/Qualifiers
     source           1. .900
                      /organism="Lycopersicon esculentum"
                      /mol_type="genomic DNA"
                      /cultivar="Heinz 1706"
                      /db_xref="taxon:4081"
                      /clone="LE_HBa0078L17"
                      /lab_host="E. coli"
                      /clone_lib="Tomato HindIII BAC Library"
                      /note="Vector: pBeloBAC11; Site_1: HindIII"
ORIGIN

  Query Match             62.4%;  Score 21.2;  DB 10;  Length 900;
  Best Local Similarity   47.1%;  Pred. No. 4.5e+02;
  Matches   16;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              | | |::|: ||| ||: :|:|:|  :|:| :||
Db        652 GTATGTTATAACAAAGTTTGTATAATTGTATTCC 685


RESULT 11
DN704358
LOCUS       DN704358                1163 bp    mRNA    linear   EST 30-MAR-2005
DEFINITION  CLJ52-H09.y1d-s SHGC-CLJ Gasterosteus aculeatus cDNA clone
            CLJ52-H09 5', mRNA sequence.
ACCESSION   DN704358
VERSION     DN704358.1  GI:62069398
KEYWORDS    EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
  ORGANISM  Gasterosteus aculeatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1  (bases 1 to 1163)
  AUTHORS   Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
            Schmutz,J. and Myers,R.M.
  TITLE     Expressed sequence tags from Gasterosteus aculeatus
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Grimwood, Jane
            Stanford Human Genome Center
            Stanford University School of Medicine
            975 S California Ave, Palo Alto, CA 94304, USA
            Tel: 650 320 5917
            Fax: 650 320 5801
            Email: jane@shgc.stanford.edu
            Plate: 52
            High quality sequence stop: 784.
FEATURES              Location/Qualifiers
     source           1. .1163
                      /organism="Gasterosteus aculeatus"
                      /mol_type="mRNA"
                      /strain="Bitrufjordur marine sticklebacks, Iceland"
                      /db_xref="taxon:69293"
                      /clone="CLJ52-H09"
                      /sex="mixed male and female"
                      /tissue_type="whole larva"
                      /dev_stage="21 day old larvae collected at Swarup Stage 30
                      (J. Embryol. Exp. Morphol 6: 373-383.1958)"
                      /lab_host="DH10B (T1 phage resistant)"
                      /clone_lib="SHGC-CLJ"
                      /note="Vector: Express 1; Total and poly A+ RNA was
                      isolated from the indicated stickleback tissue, and a cDNA
                      library was constructed in the Express 1 plasmid vector by
                      Open Biosystems. First strand cDNA synthesis was primed
                      with an 54 bp linker primer containing an oligodT sequence
                      preceeded by a synthetic NotI site (first strand primer:
                      5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3'). Following
                      second strand synthesis, cDNAs were made blunt at the end
                      corresponding to the original 5 prime end of mRNA, and
                      cloned directionally into the NotI and EcoRV sites of
                      Express 1. Note that the EcoRV site is typically destroyed
                      in the blunt end cloning, leaving a junction of the form
                      'xxxATC'(where is ATC is the second half of the EcoRV
                      site, and xxx is derived from the cDNA sequence). A map of
                      the Express 1 vector is available at:
                      http://www.openbiosystems.com/cdna_library_construction_fa
                      q.php#8 The primary library was transformed and amplified
                      in DH10B (T1 phage resistant) bacteria. Clones available
                      from Open Biosystems:
                      http://www.openbiosystems.com/stickleback"
ORIGIN

  Query Match             62.4%;  Score 21.2;  DB 8;  Length 1163;
  Best Local Similarity   47.1%;  Pred. No. 4.7e+02;
```

```
  Matches   16;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGAGGUUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ||   ::|::| |||| |:|: : ||: :||:||
Db        952 GGGTTTTATTAAAGAGCCTGTTTCGCTTTACTCC 985


RESULT 12
BZ680408
LOCUS       BZ680408                533 bp    DNA     linear   GSS 05-FEB-2003
DEFINITION  PUBGI05TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa049A09,
            genomic survey sequence.
ACCESSION   BZ680408
VERSION     BZ680408.1  GI:28235276
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .533
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa049A09"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             61.8%;  Score 21;  DB 9;  Length 533;
  Best Local Similarity   48.3%;  Pred. No. 5e+02;
  Matches   14;  Conservative   10;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 GAGGUUAUUACAGAGUCUGUAUAGCUGUA 30
              ||| :: ::|| |||:|:|: : ||:|:|
Db         30 GAGTTTGTTACGGAGTCTGTTTTGCTGTA 58


RESULT 13
CZ836446
LOCUS       CZ836446                632 bp    DNA     linear   GSS 27-JUL-2005
DEFINITION  OC__Ba0219P12.r OC__Ba Oryza coarctata genomic clone OC__Ba0219P12
            3', genomic survey sequence.
ACCESSION   CZ836446
VERSION     CZ836446.1  GI:71289972
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0219  row: P  column: 12
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Oryza coarctata"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77588"
                     /clone="OC__Ba0219P12"
                     /tissue_type="leaves"
                     /dev_stage="mature"
                     /lab_host="DH10B"
                     /clone_lib="OC__Ba"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             61.8%;  Score 21;  DB 10;  Length 632;
  Best Local Similarity   48.3%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative   10;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 UUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              :: ::|| |||: :|:|:|||  :||:||
Db        380 TTTTTACTGAGTATGTATAGCAATACTCC 408


RESULT 14
CR157585
LOCUS       CR157585                679 bp    DNA     linear   GSS 06-JUL-2004
DEFINITION  Forward strand read from insert in 5'HPRT insertion targeting and
            chromosome engineering clone MHPN356123, genomic survey sequence.
ACCESSION   CR157585
VERSION     CR157585.1  GI:49936434
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPN356123"
                     /clone_lib="MHPN"
ORIGIN

  Query Match             61.8%;  Score 21;  DB 11;  Length 679;
  Best Local Similarity   51.7%;  Pred. No. 5.2e+02;
  Matches   15;  Conservative    9;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 UUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              ::|: ||| ||:| |:|: ||:|:||: |
Db        215 TTATGACAAAGTCAGTATGGCTGTACTGC 243
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RESULT 15
AQ258623
LOCUS AQ258623 728 bp DNA linear GSS 23-OCT-1998
DEFINITION nbxb0020N10f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0020N10f, genomic survey sequence.
ACCESSION AQ258623
VERSION AQ258623.1 GI:3783105
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 728)
AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 241.
FEATURES Location/Qualifiers
source 1. .728
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0020N10f"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
ORIGIN

Query Match 61.8%; Score 21; DB 9; Length 728;
Best Local Similarity 48.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

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Qy          6 UUAUUACAGAGUCUGUAUAGCUGUACUCC 34
              :: ::|| |||:|: :|:||  |:||:||
Db        381 TTTTTACTGAGTCTATATAGACGTACTCC 409
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Search completed: December 27, 2005, 16:42:52
Job time : 3764 secs